

Patent Application US/07/952,640

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: CROWE, JAMES SCOTT
LEWIS, ALAN PETER

(ii) TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
(B) STREET: 555 THIRTEENTH ST. N.W.
(C) CITY: WASHINGTON
(D) STATE: D. C.
(E) COUNTRY: U.S.
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/952640
(B) FILING DATE: 01-DEC-1992
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: ERNST, BARBARA G
(B) REGISTRATION NUMBER: 30,377
(C) REFERENCE/DOCKET NUMBER: 1808-118

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 783-6040
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Au 1806

#8

-see p. 11, 4

32 → 37

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53
54 GACATTCAGC TGACCCAGTC TCCA 24
55
56 (2) INFORMATION FOR SEQ ID NO:2:
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58 (i) SEQUENCE CHARACTERISTICS:
59 (A) LENGTH: 24 base pairs
60 (B) TYPE: nucleic acid
61 (C) STRANDEDNESS: single
62 (D) TOPOLOGY: linear
63
64 (ii) MOLECULE TYPE: DNA (genomic)
65
66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
67
68 GATCAAGCTT CTAACACTCT CCCC 24
69
70 (2) INFORMATION FOR SEQ ID NO:3:
71
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 34 base pairs
74 (B) TYPE: nucleic acid
75 (C) STRANDEDNESS: single
76 (D) TOPOLOGY: linear
77
78 (ii) MOLECULE TYPE: DNA (genomic)
79
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
81
82 GATCAAGCTT GACATTCAGC TGACCCAGTC TCCA 34
83
84 (2) INFORMATION FOR SEQ ID NO:4:
85
86 (i) SEQUENCE CHARACTERISTICS:
87 (A) LENGTH: 16 base pairs
88 (B) TYPE: nucleic acid
89 (C) STRANDEDNESS: single
90 (D) TOPOLOGY: linear
91
92 (ii) MOLECULE TYPE: DNA (genomic)
93
94 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
95
96 AACAGCTATG ACCATG 16
97
98 (2) INFORMATION FOR SEQ ID NO:5:
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100 (i) SEQUENCE CHARACTERISTICS:
101 (A) LENGTH: 17 base pairs
102 (B) TYPE: nucleic acid
103 (C) STRANDEDNESS: single
104 (D) TOPOLOGY: linear

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105
106 (ii) MOLECULE TYPE: DNA (genomic)
107
108 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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110 GTTTTCCCAG TCACGAC 17
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112 (2) INFORMATION FOR SEQ ID NO:6:
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114 (i) SEQUENCE CHARACTERISTICS:
115 (A) LENGTH: 20 base pairs
116 (B) TYPE: nucleic acid
117 (C) STRANDEDNESS: single
118 (D) TOPOLOGY: linear
119
120 (ii) MOLECULE TYPE: DNA (genomic)
121
122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
123
124 GCGTCAGGGT GCTGCTGAGG 20
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126 (2) INFORMATION FOR SEQ ID NO:7:
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128 (i) SEQUENCE CHARACTERISTICS:
129 (A) LENGTH: 20 base pairs
130 (B) TYPE: nucleic acid
131 (C) STRANDEDNESS: single
132 (D) TOPOLOGY: linear
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134 (ii) MOLECULE TYPE: DNA (genomic)
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136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
137
138 GGCGGGAAGA TGAAGACAGA 20
139
140 (2) INFORMATION FOR SEQ ID NO:8:
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142 (i) SEQUENCE CHARACTERISTICS:
143 (A) LENGTH: 20 base pairs
144 (B) TYPE: nucleic acid
145 (C) STRANDEDNESS: single
146 (D) TOPOLOGY: linear
147
148 (ii) MOLECULE TYPE: DNA (genomic)
149
150
151
152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
153
154 TTCAGCAGGC ACACAACAGA 20
155
156 (2) INFORMATION FOR SEQ ID NO:9:

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157
158 (i) SEQUENCE CHARACTERISTICS:
159 (A) LENGTH: 1617 base pairs
160 (B) TYPE: nucleic acid
161 (C) STRANDEDNESS: both
162 (D) TOPOLOGY: linear
163
164 (ii) MOLECULE TYPE: cDNA
165
166 (iii) HYPOTHETICAL: NO
167
168 (iv) ANTI-SENSE: NO
169
170
171 (ix) FEATURE:
172 (A) NAME/KEY: sig_peptide
173 (B) LOCATION: 35..92
174
175 (ix) FEATURE:
176 (A) NAME/KEY: mat_peptide
177 (B) LOCATION: 93..1465
178
179 (ix) FEATURE:
180 (A) NAME/KEY: CDS
181 (B) LOCATION: 35..1465
182
183
184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
185
186 TCTAAAGAAG CCCCTGGGAG CACAGCTCAT CACC ATG GAC TGG ACC TGG AGG 52
187 Met Asp Trp Thr Trp Arg
188 -19 -15
189
190 TTC CTC TTT GTG GTG GCA GCA GCT ACA GGT GTC CAG TCC CAG ATG CAG 100
191 Phe Leu Phe Val Val Ala Ala Ala Thr Gly Val Gln Ser Gln Met Gln
192 -10 -5 1
193
194 GTG GTG CAG TCT GGG GCT GAA GTA AAG AAG CCT GGG TCC TCG GTG ACG 148
195 Val Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Thr
196 5 10 15
197
198 GTC TCC TGC AAG GCA TCT GGA GGC ACC TTC AGC AAC TAT GCT ATC AGC 196
199 Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr Ala Ile Ser
200 20 25 30 35
201
202 TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA GGG ATC 244
203 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile
204 40 45 50
205
206 ATC CCT CTT TTT GGT ACA CCA ACC TAC TCA CAG AAC TTC CAG GGC AGA 292
207 Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser Gln Asn Phe Gln Gly Arg
208 55 60 65

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209
210 GTC ACG ATT ACC GCG GAC AAA TCC ACC AGC ACA GCC CAC ATG GAG CTG      340
211 Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala His Met Glu Leu
212      70      75      80
213
214 ACT AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT GCG ACA GAT      388
215 Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr Asp
216      85      90      95
217
218 CGC TAC AGG CAG GCA AAT TTT GAC CGG GCC CGG GTT GGC TGG TTC GAC      436
219 Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala Arg Val Gly Trp Phe Asp
220 100      105      110      115
221
222 CCC TGG GGC CAG GGC ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG      484
223 Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
224      120      125      130
225
226 GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG      532
227 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
228      135      140      145
229
230 GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG      580
231 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
232      150      155      160
233
234 GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC      628
235 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
236      165      170      175
237
238 TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG      676
239 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
240 180      185      190      195
241
242 GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC AAC      724
243 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
244      200      205      210
245
246 GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC      772
247 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
248      215      220      225
249
250 AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA      820
251 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
252      230      235      240
253
254 CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC      868
255 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
256      245      250      255
257
258 ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC      916
259 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 260      265      270      275

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261
262   GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC           964
263   Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
264               280                     285                     290
265
266   GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC           1012
267   Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
268               295                     300                     305
269
270   AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG           1060
271   Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
272               310                     315                     320
273
274   CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA           1108
275   Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
276               325                     330                     335
277
278   GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA           1156
279   Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
280   340                     345                     350                     355
281
282   CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC           1204
283   Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
284               360                     365                     370
285
286   CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC           1252
287   Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
288               375                     380                     385
289
290   GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC           1300
291   Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
292               390                     395                     400
293
294   ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG           1348
295   Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
296               405                     410                     415
297
298   CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC           1396
299   Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
300   420                     425                     430                     435
301
302   TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC           1444
303   Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
304               440                     445                     450
305
306   TCC CTG TCT CCG GGT AAA TGAGTGCAGC GGCCGGCAAG CCCCCGCTCC           1492
307   Ser Leu Ser Pro Gly Lys
308               455
309
310   CCGGGCTCTC GCGGTGCGAC GAGGATGCTT GGCACGTACC CCGTGTACAT ACTTCCCGGG           1552
311
312   CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAAA AAAAAAAAAA           1612

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313
314 AAAAAA 1617
315 (2) INFORMATION FOR SEQ ID NO:10:
316
317 (i) SEQUENCE CHARACTERISTICS:
318 (A) LENGTH: 476 amino acids
319 (B) TYPE: amino acid
320 (D) TOPOLOGY: linear
321
322 (ii) MOLECULE TYPE: protein
323
324 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
325
326 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
327 -19 -15 -10 -5
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329 Val Gln Ser Gln Met Gln Val Val Gln Ser Gly Ala Glu Val Lys Lys
330 1 5 10
331
332 Pro Gly Ser Ser Val Thr Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
333 15 20 25
334
335 Ser Asn Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
336 30 35 40 45
337
338 Glu Trp Met Gly Gly Ile Ile Pro Leu Phe Gly Thr Pro Thr Tyr Ser
339 50 55 60
340
341 Gln Asn Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
342 65 70 75
343
344 Thr Ala His Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val
345 80 85 90
346
347 Tyr Tyr Cys Ala Thr Asp Arg Tyr Arg Gln Ala Asn Phe Asp Arg Ala
348 95 100 105
349
350 Arg Val Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val
351 110 115 120 125
352
353 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
354 130 135 140
355
356 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
357 145 150 155
358
359 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
360 160 165 170
361
362 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
363 175 180 185
364

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365 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
366 190 195 200 205
367
368 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
369 210 215 220
370
371 Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
372 225 230 235
373
374 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
375 240 245 250
376
377 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
378 255 260 265
379
380 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
381 270 275 280 285
382
383 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
384 290 295 300
385
386 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
387 305 310 315
388
389 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
390 320 325 330
391
392 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
393 335 340 345
394
395 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
396 350 355 360 365
397
398 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
399 370 375 380
400
401 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
402 385 390 395
403
404 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
405 400 405 410
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407 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
408 415 420 425
409
410 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
411 430 435 440 445
412
413 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
414 450 455
415
416

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417 (2) INFORMATION FOR SEQ ID NO:11:

418

419 (i) SEQUENCE CHARACTERISTICS:

420 (A) LENGTH: 902 base pairs

421 (B) TYPE: nucleic acid

422 (C) STRANDEDNESS: both

423 (D) TOPOLOGY: linear

424

425 (ii) MOLECULE TYPE: cDNA

426

427 (iii) HYPOTHETICAL: NO

428

429 (iv) ANTI-SENSE: NO

430

431

432 (ix) FEATURE:

433 (A) NAME/KEY: CDS

434 (B) LOCATION: 32..739

435

436 (ix) FEATURE:

437 (A) NAME/KEY: mat_peptide

438 (B) LOCATION: 89..739

439

440 (ix) FEATURE:

441 (A) NAME/KEY: sig_peptide

442 (B) LOCATION: 32..86

443

444

445 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

446

447 CAAGAGGCAG CGCTCTCGGG ACGTCTCCAC C ATG GCC TGG GCT CTG CTG CTC 52

448 Met Ala Trp Ala Leu Leu Leu

449 -19 -15

450

451 CTC ACC CTC CTC ACT CAG GAC ACA GGG TCC TGG GCC CAG TCT GCC CTG 100

452 Leu Thr Leu Leu Thr Gln Asp Thr Gly Ser Trp Ala Gln Ser Ala Leu

453 -10 -5 1

454

455 ACT CAG CCT GCC TCC GTG TCT GGG TCT CCT GGA CAG TCG ATC ACC ATC 148

456 Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile

457 5 10 15 20

458

459 TCC TGC ACT GGA ACC AAC AAT GAT GTT GGG AGT TAT AAC CTT GTC TCC 196

460 Ser Cys Thr Gly Thr Asn Asn Asp Val Gly Ser Tyr Asn Leu Val Ser

461 25 30 35

462

463 TGG TAC CAG CAG CAC CCA GGC AAA GCC CCC AAA ATC ATG ATT TAT GAG 244

464 Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Ile Met Ile Tyr Glu

465 40 45 50

466

467 GTC AGT AAG CGG CCC TCA GGG GTT TCT AAT CGC TTC TCT GGC TCC AAG 292

468 Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys

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	55	60	65	
469				
470				
471	TCT GGC AAC ACG GCC TCC CTG ACA ATC TCT GGG CTC CAG GCT GAG GAC			340
472	Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp			
473	70	75	80	
474				
475	GAG GCT GAT TAT TAC TGC TGC TCA TAT GCA GGT AGT TAC ACT GTG GTT			388
476	Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser Tyr Thr Val Val			
477	85	90	95	100
478				
479	TTC GGC GGA GGG ACC AAA CTG ACC GTC CTA GGT CAG CCC AAG GCT GCC			436
480	Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala			
481	105	110	115	
482				
483	CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG CTT CAA GCC AAC			484
484	Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn			
485	120	125	130	
486				
487	AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG			532
488	Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val			
489	135	140	145	
490				
491	ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG			580
492	Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu			
493	150	155	160	
494				
495	ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC			628
496	Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser			
497	165	170	175	180
498				
499	TAT CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC			676
500	Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser			
501	185	190	195	
502				
503	TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT			724
504	Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro			
505	200	205	210	
506				
507	ACA GAA TGT TCA TAGGTTCTAA ACCCTCACCC CCCCCACGGG AGACTAGAGC			776
508	Thr Glu Cys Ser			
509	215			
510				
511	TGCAGGATCC CAGGGGAGGG GTCTCTCCTC CCACCCCAAG GCATCAAGCC CTTCTCCCTG			836
512				
513	CACTCAATAA ACCCTCAATA AATATTCTCA TTGTCAATCA CAAAAAAAAA AAAAAAAAAA			896
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515	AAAAAA			902
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518	(2) INFORMATION FOR SEQ ID NO:12:			
519				
520	(i) SEQUENCE CHARACTERISTICS:			

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521 (A) LENGTH: 235 amino acids
522 (B) TYPE: amino acid
523 (D) TOPOLOGY: linear
524
525 (ii) MOLECULE TYPE: protein
526
527 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
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529 Met Ala Trp Ala Leu Leu Leu Thr Leu Leu Thr Gln Asp Thr Gly
530 -19 -15 -10 -5
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532 Ser Trp Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
533 1 5 10
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535 Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Asn Asn Asp Val
536 15 20 25
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538 Gly Ser Tyr Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
539 30 35 40 45
540
541 Pro Lys Ile Met Ile Tyr Glu Val Ser Lys Arg Pro Ser Gly Val Ser
542 50 55 60
543
544 Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
545 65 70 75
546
547 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
548 80 85 90
549
550 Ala Gly Ser Tyr Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
551 95 100 105
552
553 Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser
554 110 115 120 125
555
556 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
557 130 135 140
558
559 Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
560 145 150 155
561
562 Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
563 160 165 170
564
565 Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
566 175 180 185
567
568 Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
569 190 195 200 205
570
571 Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
572 210 215

(2) INFORMATION FOR SEQ ID NO:13:

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if present).

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573
574 (i) SEQUENCE CHARACTERISTICS:
575 (A) LENGTH: 321 base pairs
576 (B) TYPE: nucleic acid
577 (C) STRANDEDNESS: both
578 (D) TOPOLOGY: linear
579
580 (ii) MOLECULE TYPE: cDNA
581
582 (iii) HYPOTHETICAL: NO
583
584 (iv) ANTI-SENSE: NO
585
586
587 (ix) FEATURE:
588 (A) NAME/KEY: CDS
589 (B) LOCATION: 1..321
590
591
592 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
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594 GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA 48
595 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
596 1 5 10 15
597
598 GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT 96
599 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
600 20 25 30
601
602 TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC 144
603 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
604 35 40 45
605
606 TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC ACA TCA AGG TTC AGT GGC 192
607 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
608 50 55 60
609
610 AGT GGA TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT 240
611 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
612 65 70 75 80
613
614 GAA GAT TCT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG ATC 288
615 Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
616 85 90 95
617
618 ACC TTC GGC CAA GGG ACA CGA CTG GAG ATT AAA 321
619 Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
620 100 105
621
622
623 (2) INFORMATION FOR SEQ ID NO:14:
624

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625 (i) SEQUENCE CHARACTERISTICS:
626 (A) LENGTH: 107 amino acids
627 (B) TYPE: amino acid
628 (D) TOPOLOGY: linear
629
630 (ii) MOLECULE TYPE: protein
631
632 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
633
634 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
635 1 5 10 15
636
637 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
638 20 25 30
639
640 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
641 35 40 45
642
643 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Thr Ser Arg Phe Ser Gly
644 50 55 60
645
646 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
647 65 70 75 80
648
649 Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Ile
650 85 90 95
651
652 Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
653 100 105
654
655 (2) INFORMATION FOR SEQ ID NO:15:
656
657 (i) SEQUENCE CHARACTERISTICS:
658 (A) LENGTH: 324 base pairs
659 (B) TYPE: nucleic acid
660 (C) STRANDEDNESS: both
661 (D) TOPOLOGY: linear
662
663 (ii) MOLECULE TYPE: cDNA
664
665 (iii) HYPOTHETICAL: NO
666
667 (iv) ANTI-SENSE: NO
668
669
670 (ix) FEATURE:
671 (A) NAME/KEY: CDS
672 (B) LOCATION: 1..324
673
674
675 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
676

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677 GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA      48
678 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
679   1               5               10               15
680
681 GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT      96
682 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
683           20               25               30
684
685 TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT GAG CTC CTG ATC      144
686 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
687           35               40               45
688
689 TAT GCT GCT TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC      192
690 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
691   50               55               60
692
693 AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT      240
694 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
695   65               70               75               80
696
697 GAA GAT TCT GCA GTT TAT TAC TGT CAA CAC ACT TAT AGT GAC CCG TAC      288
698 Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
699           85               90               95
700
701 AGT TTT GGC CAG GGG ACC AAA GTG GAC ATC AAA CGA      324
702 Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
703           100               105
704
705
706 (2) INFORMATION FOR SEQ ID NO:16:
707
708 (i) SEQUENCE CHARACTERISTICS:
709 (A) LENGTH: 108 amino acids
710 (B) TYPE: amino acid
711 (D) TOPOLOGY: linear
712
713 (ii) MOLECULE TYPE: protein
714
715 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
716
717 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
718   1               5               10               15
719
720 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
721           20               25               30
722
723 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
724           35               40               45
725
726 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
727   50               55               60
728

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729 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 730 65 70 75 80
 731
 732 Glu Asp Ser Ala Val Tyr Tyr Cys Gln His Thr Tyr Ser Asp Pro Tyr
 733 85 90 95
 734
 735 Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg
 736 100 105
 737

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

759
 760 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCT TCT GTA GGA 48
 761 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 762 1 5 10 15
 763
 764 GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGC ACT TAT 96
 765 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
 766 20 25 30
 767
 768 TTA AGT TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC 144
 769 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 770 35 40 45
 771
 772 TAT TAT GCA AAC AGT TTG GCA AGT GGG GTC CCA TCA AGG TTC AGC GGC 192
 773 Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 774 50 55 60
 775
 776 AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240
 777 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 778 65 70 75 80
 779
 780 GAA GAT TCT GCA ACT TAT TAC TGT GGA CAG GGT AAT AGT TAC CCT CTC 288

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781 Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu
782 85 90 95

783
784 ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324
785 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
786 100 105

787
788

789 (2) INFORMATION FOR SEQ ID NO:18:

790

791 (i) SEQUENCE CHARACTERISTICS:

792 (A) LENGTH: 108 amino acids

793 (B) TYPE: amino acid

794 (D) TOPOLOGY: linear

795

796 (ii) MOLECULE TYPE: protein

797

798 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

799

800 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
801 1 5 10 15

802

803 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Tyr
804 20 25 30

805

806 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
807 35 40 45

808

809 Tyr Tyr Ala Asn Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
810 50 55 60

811

812 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
813 65 70 75 80

814

815 Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Asn Ser Tyr Pro Leu
816 85 90 95

817

818 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
819 100 105

820

821 (2) INFORMATION FOR SEQ ID NO:19:

822

823 (i) SEQUENCE CHARACTERISTICS:

824 (A) LENGTH: 324 base pairs

825 (B) TYPE: nucleic acid

826 (C) STRANDEDNESS: both

827 (D) TOPOLOGY: linear

828

829 (ii) MOLECULE TYPE: cDNA

830

831 (iii) HYPOTHETICAL: NO

832

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833 (iv) ANTI-SENSE: NO

834

835

836 (ix) FEATURE:

837 (A) NAME/KEY: CDS

838 (B) LOCATION: 1..324

839

840

841 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

842

843 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCT CAG TCT GCA TCT GTA GGA 48

844 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly

845 1 5 10 15

846

847 GAC AGA GTG ACC ATT ACT TGC CAG GCG AGT CAA AGC CTT AGC AAT TAT 96

848 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr

849 20 25 30

850

851 TTA AAT TGG TAT CAG CAG AAA CCA GGG AAA ATT CCT AAG CTC CTG ATC 144

852 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile

853 35 40 45

854

855 TAT AGG GCA TCC AGT TTG CAA AGT GGG ATT CCC TCT CGG TTC AGC GGC 192

856 Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly

857 50 55 60

858

859 AGT GGA TCT GGG ACG GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240

860 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

861 65 70 75 80

862

863 GAA GAT TTT GCC ACT TAT TAC TGT CAG CAT AAT TAT GGT ACC CCT CTC 288

864 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu

865 85 90 95

866

867 ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324

868 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg

869 100 105

870

871

872 (2) INFORMATION FOR SEQ ID NO:20:

873

874 (i) SEQUENCE CHARACTERISTICS:

875 (A) LENGTH: 108 amino acids

876 (B) TYPE: amino acid

877 (D) TOPOLOGY: linear

878

879 (ii) MOLECULE TYPE: protein

880

881 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

882

883 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Gln Ser Ala Ser Val Gly

884 1 5 10 15

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885
886 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Leu Ser Asn Tyr
887 20 25 30
888
889 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ile Pro Lys Leu Leu Ile
890 35 40 45
891
892 Tyr Arg Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
893 50 55 60
894
895 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
896 65 70 75 80
897
898 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Asn Tyr Gly Thr Pro Leu
899 85 90 95
900
901 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
902 100 105
903

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

921 GACATTCAGC TGACCCAGTC TCCACTCTCC CTGCCCCGTCA GTCTTGGAGA GTCGGCCTCC 60
922
923 ATCTCCTNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120
924
925 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNTCCCAGAC 180
926
927 AGGTTCAC TG CAGTGGGTC AGGCACTGAT TTCACACTGA AAATCAGCAG AGTGGAGGCT 240
928
929 GAGGATGTTG GGGTTTATTA CTGCATGCAA GCTCTTCGGT CTCCTTGGAC GTTCGGCCAA 300
930
931 GGGACCAAGG TGGAAATCAG ACGA 324
932
933

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

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937 (A) LENGTH: 108 amino acids
938 (B) TYPE: amino acid
939 (D) TOPOLOGY: linear
940

941 (ii) MOLECULE TYPE: protein
942

943 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
944

945 Asp Ile Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
946 1 5 10 15
947
948 Glu Ser Ala Ser Ile Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
949 20 25 30
950
951 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
952 35 40 45
953
954 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Asp Xaa Xaa Thr Xaa
955 50 55 60
956
957 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Arg Val Glu Ala
958 65 70 75 80
959
960 Xaa Xaa Val Gly Val Xaa Xaa Xaa Met Xaa Ala Leu Arg Ser Pro Trp
961 85 90 95
962
963 Xaa Xaa Xaa Xaa Xaa Xaa Lys Val Xaa Xaa Arg Arg
964 100 105
965
966

967 (2) INFORMATION FOR SEQ ID NO:23:
968

969 (i) SEQUENCE CHARACTERISTICS:
970 (A) LENGTH: 324 base pairs
971 (B) TYPE: nucleic acid
972 (C) STRANDEDNESS: both
973 (D) TOPOLOGY: linear
974

975 (ii) MOLECULE TYPE: cDNA
976

977 (iii) HYPOTHETICAL: NO
978

979 (iv) ANTI-SENSE: NO
980

981 (ix) FEATURE:
982

983 (A) NAME/KEY: CDS
984 (B) LOCATION: 1..324
985

986
987 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
988

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989 GAC ATT CAG CTG ACC CAG TCT CCA TCT TCC CTG TCT GCA TCG GTA GGA      48
990 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
991   1               5               10               15
992
993 GAC AGA GTC ACC ATC ACC TGC AGG GCA AGT CAG GGC ATT AGC GAT TAT      96
994 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
995   20               25               30
996
997 TTA AGT TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CTC CTG ATC      144
998 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
999   35               40               45
1000
1001 TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC      192
1002 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1003   50               55               60
1004
1005 AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAA CCT      240
1006 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1007   65               70               75               80
1008
1009 GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG GGT TAT GGT ACC CCG TAC      288
1010 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
1011   85               90               95
1012
1013 AGT TTT GGC CAG GGG ACC AAA GTG GAG ATC AAA CGA      324
1014 Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1015   100               105
1016
1017
1018 (2) INFORMATION FOR SEQ ID NO:24:
1019
1020 (i) SEQUENCE CHARACTERISTICS:
1021 (A) LENGTH: 108 amino acids
1022 (B) TYPE: amino acid
1023 (D) TOPOLOGY: linear
1024
1025 (ii) MOLECULE TYPE: protein
1026
1027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
1028
1029 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1030   1               5               10               15
1031
1032 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asp Tyr
1033   20               25               30
1034
1035 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1036   35               40               45
1037
1038 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
1039   50               55               60
1040
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1041 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1042 65 70 75 80
1043
1044 Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly Tyr Gly Thr Pro Tyr
1045 85 90 95
1046
1047 Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1048 100 105
1049

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

1071
1072 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA 48
1073 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1074 1 5 10 15
1075
1076 GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GAC ATT AGC AAT AAT 96
1077 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
1078 20 25 30
1079
1080 TTA GTC TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC 144
1081 Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1082 35 40 45
1083
1084 TAT GCT GCA TCC AGA TTG CAA GAT GGG GTC CCA TCA AGG TTC AGC GGC 192
1085 Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
1086 50 55 60
1087
1088 AGT GGG TCT GGG ACC GAT TTC ACC CTC ACA ATT AAT CCT GTG GAA GCT 240
1089 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
1090 65 70 75 80
1091
1092 GAC GAT GCT GCG GAT TAC TAC TGT CTA CAG ACT AAG AGT TCT CCT CGG 288

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1093 Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg
1094 85 90 95
1095
1096 ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGA
1097 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1098 100 105
1099
1100

324

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

1111
1112 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1113 1 5 10 15
1114
1115 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Asn
1116 20 25 30
1117
1118 Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1119 35 40 45
1120
1121 Tyr Ala Ala Ser Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
1122 50 55 60
1123
1124 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala
1125 65 70 75 80
1126
1127 Asp Asp Ala Ala Asp Tyr Tyr Cys Leu Gln Thr Lys Ser Ser Pro Arg
1128 85 90 95
1129
1130 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
1131 100 105
1132

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

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1145 (A) NAME/KEY: CDS
1146 (B) LOCATION: 1..324
1147
1148 (ix) FEATURE:
1149 (A) NAME/KEY: mat_peptide
1150 (B) LOCATION: 31..324
1151
1152
1153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
1154
1155 GACATTCAGC TGACCCAGTC TCCANNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 60
1156
1157 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 120
1158
1159 NNNNNNNNNN NNCAGCCCTT GATTTATGAG GTTTCACACC GGGCCTCTGG AGTCCCAGAC 180
1160
1161 AGGTTTCAGTG GCAGTGGGTC GGACACTGAT TTCACACTCA AAATCAGCAG AGTGGAGGCT 240
1162
1163 GAGGATGTTG GGGTTTATTA CTGCATGCAA TATACACACA TTCCATTCAC TTTCGGCCCC 300
1164
1165 GGGACCAAAC TGGATATCAA ACGA 324
1166
1167 (2) INFORMATION FOR SEQ ID NO:28:
1168
1169 (i) SEQUENCE CHARACTERISTICS:
1170 (A) LENGTH: 108 amino acids
1171 (B) TYPE: amino acid
1172 (D) TOPOLOGY: linear
1173
1174 (ii) MOLECULE TYPE: protein
1175
1176
1177
1178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
1179
1180 Asp Ile Gln Leu Thr Gln Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1181 1 5 10 15
1182
1183 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1184 20 25 30
1185
1186 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Pro Leu Ile
1187 35 40 45
1188
1189 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1190 50 55 60
1191
1192 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1193 65 70 75 80
1194
1195 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1196 85 90 95

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1197
1198 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1199 100 105
1200
1201
1202
1203
1204 (2) INFORMATION FOR SEQ ID NO:29:
1205
1206 (i) SEQUENCE CHARACTERISTICS:
1207 (A) LENGTH: 324 base pairs
1208 (B) TYPE: nucleic acid
1209 (C) STRANDEDNESS: both
1210 (D) TOPOLOGY: linear
1211
1212 (ii) MOLECULE TYPE: cDNA
1213
1214 (iii) HYPOTHETICAL: NO
1215
1216 (iv) ANTI-SENSE: NO
1217
1218
1219 (ix) FEATURE:
1220 (A) NAME/KEY: CDS
1221 (B) LOCATION: 1..324
1222
1223
1224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
1225
1226 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA 48
1227 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1228 1 5 10 15
1229
1230 GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AAT TAT 96
1231 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
1232 20 25 30
1233
1234 TTA AAT TGG TAT CAA CAG AAA CCA GGG AAA GCC CCT CAG CCC TTG ATT 144
1235 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile
1236 35 40 45
1237
1238 TAT GAG GTT TCC AAC CGG GCC TCT GGA GTC CCA GAC AGG TTC AGT GGC 192
1239 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1240 50 55 60
1241
1242 AGT GGG TCG GAC ACT GAT TTC ACA CTC AAA ATC AGC AGA GTG GAG GCT 240
1243 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1244 65 70 75 80
1245
1246 GAG GAT GTT GGG GTT TAT TAC TGC ATG CAA TAT ACA CAC ATT CCA TTC 288
1247 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1248 85 90 95

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1249
1250 ACT TTC GGC CCC GGG ACC AAA CTG GAT ATC AAA CGA 324
1251 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1252 100 105
1253
1254
1255 (2) INFORMATION FOR SEQ ID NO:30:
1256
1257 (i) SEQUENCE CHARACTERISTICS:
1258 (A) LENGTH: 108 amino acids
1259 (B) TYPE: amino acid
1260 (D) TOPOLOGY: linear
1261
1262 (ii) MOLECULE TYPE: protein
1263
1264 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
1265
1266 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1267 1 5 10 15
1268
1269 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
1270 20 25 30
1271
1272 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Gln Pro Leu Ile
1273 35 40 45
1274
1275 Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
1276 50 55 60
1277
1278 Ser Gly Ser Asp Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
1279 65 70 75 80
1280
1281 Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Tyr Thr His Ile Pro Phe
1282 85 90 95
1283
1284 Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys Arg
1285 100 105
1286
1287 (2) INFORMATION FOR SEQ ID NO:31
1288
1289 (i) SEQUENCE CHARACTERISTICS:
1290 (A) LENGTH: 324 base pairs
1291 (B) TYPE: nucleic acid
1292 (C) STRANDEDNESS: both
1293 (D) TOPOLOGY: linear
1294
1295 (ii) MOLECULE TYPE: cDNA
1296
1297 (iii) HYPOTHETICAL: NO
1298
1299 (iv) ANTI-SENSE: NO
1300

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1301
1302 (ix) FEATURE:
1303 (A) NAME/KEY: CDS
1304 (B) LOCATION: 1..324
1305
1306
1307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31
1308
1309 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA 48
1310 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1311 1 5 10 15
1312
1313 GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GGC ATT AGC AAT AAT 96
1314 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1315 20 25 30
1316
1317 TTA GCC TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CGC CTG ATC 144
1318 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1319 35 40 45
1320
1321 TAT GCT GCA TCC AGT TTG GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC 192
1322 Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1323 50 55 60
1324
1325 AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240
1326 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1327 65 70 75 80
1328
1329 GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG GAT AAC AGT TAT CCT TTC 288
1330 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1331 85 90 95
1332
1333 ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324
1334 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1335 100 105
1336
1337
1338 (2) INFORMATION FOR SEQ ID NO:32
1339
1340 (i) SEQUENCE CHARACTERISTICS:
1341 (A) LENGTH: 108 amino acids
1342 (B) TYPE: amino acid
1343 (D) TOPOLOGY: linear
1344
1345 (ii) MOLECULE TYPE: protein
1346
1347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32
1348
1349 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1350 1 5 10 15
1351
1352 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn

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1353 20 25 30
1354
1355 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1356 35 40 45
1357
1358 Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1359 50 55 60
1360
1361 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1362 65 70 75 80
1363
1364 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1365 85 90 95
1366
1367 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1368 100 105
1369
1370 (2) INFORMATION FOR SEQ ID NO:33
1371
1372 (i) SEQUENCE CHARACTERISTICS:
1373 (A) LENGTH: 324 base pairs
1374 (B) TYPE: nucleic acid
1375 (C) STRANDEDNESS: both
1376 (D) TOPOLOGY: linear
1377
1378 (ii) MOLECULE TYPE: cDNA
1379
1380 (iii) HYPOTHETICAL: NO
1381
1382 (iv) ANTI-SENSE: NO
1383
1384
1385 (ix) FEATURE:
1386 (A) NAME/KEY: CDS
1387 (B) LOCATION: 1..324
1388
1389
1390 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33
1391
1392 GAC ATT CAG CTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA 48
1393 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1394 1 5 10 15
1395
1396 GAC ACA GTC ACC ATC ACT TGT CGG GCA AGT CAG GGC ATT AGC AAT AAT 96
1397 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1398 20 25 30
1399
1400 TTA GCC TGG TAT CAG CAG AAA CCA GGA AAA GCT CCT AAG CGC CTG ATC 144
1401 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1402 35 40 45
1403
1404 TAT GCT GCA TCC AGT TTG GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC 192

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1405 Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1406 50 55 60
1407
1408 AGT GGA TCT GGG ACA GAA TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT 240
1409 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1410 65 70 75 80
1411
1412 GAA GAT TTT GCA ACT TAT TAC TGT CAA CAG GAT AAC AGT TAT CCT TTC 288
1413 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1414 85 90 95
1415
1416 ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA 324
1417 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1418 100 105
1419
1420
1421 (2) INFORMATION FOR SEQ ID NO:34
1422
1423 (i) SEQUENCE CHARACTERISTICS:
1424 (A) LENGTH: 108 amino acids
1425 (B) TYPE: amino acid
1426 (D) TOPOLOGY: linear
1427
1428 (ii) MOLECULE TYPE: protein
1429
1430 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34
1431
1432 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1433 1 5 10 15
1434
1435 Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
1436 20 25 30
1437
1438 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1439 35 40 45
1440
1441 Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
1442 50 55 60
1443
1444 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
1445 65 70 75 80
1446
1447 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Asn Ser Tyr Pro Phe
1448 85 90 95
1449
1450 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1451 100 105
1452
1453 (2) INFORMATION FOR SEQ ID NO:35:
1454
1455 (i) SEQUENCE CHARACTERISTICS:
1456 (A) LENGTH: 342 base pairs

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1457 (B) TYPE: nucleic acid
1458 (C) STRANDEDNESS: both
1459 (D) TOPOLOGY: linear
1460
1461 (ii) MOLECULE TYPE: cDNA
1462
1463
1464 (ix) FEATURE:
1465 (A) NAME/KEY: CDS
1466 (B) LOCATION: 1..342
1467
1468
1469 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
1470
1471 GAC ATT GTG ATG ACT CAG TCT CCA ACT TTC CTT GCT GTG ACA GCA AGT 48
1472 Asp Ile Val Met Thr Gln Ser Pro Thr Phe Leu Ala Val Thr Ala Ser
1473 1 5 10 15
1474
1475 AAG AAG GTC ACC ATT AGT TGC ACT GCC TCT GAG AGC CTT TAT TCA AGC 96
1476 Lys Lys Val Thr Ile Ser Cys Thr Ala Ser Glu Ser Leu Tyr Ser Ser
1477 20 25 30
1478
1479 AAA CAC AAG GTG CAC TAC TTG GCT TGG TAC CAG AAG AAA CCA GAG CAA 144
1480 Lys His Lys Val His Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Glu Gln
1481 35 40 45
1482
1483 TCT CCT AAA CTG CTG ATA TAC GGG GCA TCC AAC CGA TAC ATT GGG GTC 192
1484 Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Ile Gly Val
1485 50 55 60
1486
1487 CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTG ACC 240
1488 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1489 65 70 75 80
1490
1491 ATC AGC AGT GTA CAG GTT GAA GAC CTC ACA CAT TAT TAC TGT GCA CAG 288
1492 Ile Ser Ser Val Gln Val Glu Asp Leu Thr His Tyr Tyr Cys Ala Gln
1493 85 90 95
1494
1495 TTT TAC AGC TAT CCT CTC ACG TTC GGT GCT GGG ACC AAG CTG GAG CTG 336
1496 Phe Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
1497 100 105 110
1498
1499 AAA CGG 342
1500 Lys Arg
1501
1502
1503
1504 (2) INFORMATION FOR SEQ ID NO:36:
1505
1506 (i) SEQUENCE CHARACTERISTICS:
1507 (A) LENGTH: 114 amino acids
1508 (B) TYPE: amino acid

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1509 (D) TOPOLOGY: linear
1510
1511 (ii) MOLECULE TYPE: protein
1512
1513 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
1514
1515 Asp Ile Val Met Thr Gln Ser Pro Thr Phe Leu Ala Val Thr Ala Ser
1516 1 5 10 15
1517
1518 Lys Lys Val Thr Ile Ser Cys Thr Ala Ser Glu Ser Leu Tyr Ser Ser
1519 20 25 30
1520
1521 Lys His Lys Val His Tyr Leu Ala Trp Tyr Gln Lys Lys Pro Glu Gln
1522 35 40 45
1523
1524 Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Ile Gly Val
1525 50 55 60
1526
1527 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
1528 65 70 75 80
1529
1530 Ile Ser Ser Val Gln Val Glu Asp Leu Thr His Tyr Tyr Cys Ala Gln
1531 85 90 95
1532
1533 Phe Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
1534 100 105 110
1535
1536 Lys Arg
1537
1538
1539 (2) INFORMATION FOR SEQ ID NO:37:
1540
1541 (i) SEQUENCE CHARACTERISTICS:
1542 (A) LENGTH: 327 base pairs
1543 (B) TYPE: nucleic acid
1544 (C) STRANDEDNESS: both
1545 (D) TOPOLOGY: linear
1546
1547 (ii) MOLECULE TYPE: cDNA
1548
1549 (iii) HYPOTHETICAL: NO
1550
1551 (iv) ANTI-SENSE: NO
1552
1553
1554 (ix) FEATURE:
1555 (A) NAME/KEY: CDS
1556 (B) LOCATION: 1..327
1557
1558
1559 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37
1560

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1561 GCC CTC GTG ATG ACC CAG ACT CCA GCC TCC GTG TCT GCA GCT GTG GGA      48
1562 Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1563   1                      5                      10                      15
1564
1565 GGC ACA GTC ACC ATC AAG TGC CAG GCC AGT GAG AAC ATT TAC AGC TCT      96
1566 Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Asn Ile Tyr Ser Ser
1567           20                      25                      30
1568
1569 TTA GCC TGG TAT CAG CAG AAA CCA GGG CAG CCT CCC AAG CTC CTG ATC      144
1570 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1571       35                      40                      45
1572
1573 TAT GGT GCA TCC ACT CTG GCA TCT GGG GTC CCA TCG CGG TTC AAA GGC      192
1574 Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
1575       50                      55                      60
1576
1577 AGT AGA TCT GGG ACA GAG TAC ACT CTC ACC ATC AGC GGC GTG CAG CGT      240
1578 Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg
1579   65                      70                      75                      80
1580
1581 GAG GAT GCT GCC ACC TAC TAC TGT CTA GGC AGT GAT AGT AGT AGC GAT      288
1582 Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Asp Ser Ser Ser Asp
1583           85                      90                      95
1584
1585 ACT GCT TTC GGC GGA GGG ACC GAG CTG GAG ATC CTA TGT      327
1586 Thr Ala Phe Gly Gly Thr Glu Leu Glu Ile Leu Cys
1587       100                      105
1588
1589
1590 (2) INFORMATION FOR SEQ ID NO:38:
1591
1592 (i) SEQUENCE CHARACTERISTICS:
1593 (A) LENGTH: 109 amino acids
1594 (B) TYPE: amino acid
1595 (D) TOPOLOGY: linear
1596
1597 (ii) MOLECULE TYPE: protein
1598
1599 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
1600
1601 Ala Leu Val Met Thr Gln Thr Pro Ala Ser Val Ser Ala Ala Val Gly
1602   1                      5                      10                      15
1603
1604 Gly Thr Val Thr Ile Lys Cys Gln Ala Ser Glu Asn Ile Tyr Ser Ser
1605       20                      25                      30
1606
1607 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
1608       35                      40                      45
1609
1610 Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Lys Gly
1611       50                      55                      60
1612
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1613 Ser Arg Ser Gly Thr Glu Tyr Thr Leu Thr Ile Ser Gly Val Gln Arg
1614 65 70 75 80
1615
1616 Glu Asp Ala Ala Thr Tyr Tyr Cys Leu Gly Ser Asp Ser Ser Ser Asp
1617 85 90 95
1618
1619 Thr Ala Phe Gly Gly Gly Thr Glu Leu Glu Ile Leu Cys
1620 100 105
1621

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

1643
1644 ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG 48
1645 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1646 1 5 10 15
1647
1648 TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT 96
1649 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1650 20 25 30
1651
1652 CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG 144
1653 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
1654 35 40 45
1655
1656 GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC 192
1657 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
1658 50 55 60
1659
1660 TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 240
1661 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
1662 65 70 75 80
1663
1664 CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC 288

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1665 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1666 85 90 95
1667
1668 GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TA
1669 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1670 100 105
1671
1672

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

1684 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1685 1 5 10 15
1686
1687 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1688 20 25 30
1689
1690 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
1691 35 40 45
1692
1693 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
1694 50 55 60
1695
1696 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
1697 65 70 75 80
1698
1699 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1700 85 90 95
1701
1702 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1703 100 105
1704
1705

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

321

320
are listed
on this line

320 listed

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1717
1718 (iv) ANTI-SENSE: NO
1719
1720
1721 (ix) FEATURE:
1722 (A) NAME/KEY: CDS
1723 (B) LOCATION: 1..321
1724
1725
1726 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
1727
1728 GCT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAG GAT CAG 48
1729 Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln
1730 1 5 10 15
1731
1732 GTG AAA TCT GGA ACT GTC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT 96
1733 Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1734 20 25 30
1735
1736 CCC AGA GAG GCC AGC GTA AAG TGG AAG GTG GAT GGT GCC CTC AAA ACG 144
1737 Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
1738 35 40 45
1739
1740 GAT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AAC ACC 192
1741 Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
1742 50 55 60
1743
1744 TAC AGC CTG AGC AGC ACC CTG ACG CTG AGC AGC ACA GAC TAC CAG AGT 240
1745 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
1746 65 70 75 80
1747
1748 CAC AAT GTC TAT GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC 288
1749 His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1750 85 90 95
1751
1752 GTC ACC AAG AGC TTC AAC AGG GGA GAG TGT TA
1753 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1754 100 105
1755
1756
1757 (2) INFORMATION FOR SEQ ID NO:42:
1758
1759 (i) SEQUENCE CHARACTERISTICS:
1760 (A) LENGTH: 106 amino acids
1761 (B) TYPE: amino acid
1762 (D) TOPOLOGY: linear
1763
1764 (ii) MOLECULE TYPE: protein
1765
1766 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
1767
1768 Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Glu Asp Gln

321

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1769      1              5              10              15
1770
1771 Val Lys Ser Gly Thr Val Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
1772                20                25                30
1773
1774 Pro Arg Glu Ala Ser Val Lys Trp Lys Val Asp Gly Ala Leu Lys Thr
1775          35          40          45
1776
1777 Asp Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Asn Thr
1778      50              55              60
1779
1780 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Ser Thr Asp Tyr Gln Ser
1781      65              70              75              80
1782
1783 His Asn Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
1784                85                90                95
1785
1786 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
1787          100          105
1788
1789

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(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

320 listed

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

1811
1812 GAT CCA ATT GCG CCT ACT GTC CTC CTC TTC CCA CCA TCT GCT GAT CAG      48
1813 Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln
1814      1              5              10              15
1815
1816 CTG ACA ACT GAA ACA GTC ACC ATC GTG TGC GTG GCA AAT AAA TTC CGT      96
1817 Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg
1818          20          25          30
1819
1820 CCC AAT GAC ATC ACC GTC ACC TGG AAG GTG GAT GAC GAA ATC CAA CAG      144

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1821 Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln
1822 35 40 45
1823
1824 AGC GGC TTC GAG AAC AGT ACA ACA CCG CAG AGC CCC GAG GAC TGT ACC 192
1825 Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr
1826 50 55 60
1827
1828 TAC AAC CTC AGC AGC ACT CTG TCA CTG ACC AAA GCA CAG TAC AAC AGC 240
1829 Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser
1830 65 70 75 80
1831
1832 CAC AGC GTG TAC ACC TGC GAG GTG GTC CAT CAC AAC TCG GGC TCA GCG 288
1833 His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala
1834 85 90 95
1835
1836 ATC GTC CAG AGC TTC AAT AGG GGT GAC TGT TA
1837 Ile Val Gln Ser Phe Asn Arg Gly Asp Cys
1838 100 105
1839
1840
1841 (2) INFORMATION FOR SEQ ID NO:44:
1842
1843 (i) SEQUENCE CHARACTERISTICS:
1844 (A) LENGTH: 106 amino acids
1845 (B) TYPE: amino acid
1846 (D) TOPOLOGY: linear
1847
1848 (ii) MOLECULE TYPE: protein
1849
1850 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
1851
1852 Asp Pro Ile Ala Pro Thr Val Leu Leu Phe Pro Pro Ser Ala Asp Gln
1853 1 5 10 15
1854
1855 Leu Thr Thr Glu Thr Val Thr Ile Val Cys Val Ala Asn Lys Phe Arg
1856 20 25 30
1857
1858 Pro Asn Asp Ile Thr Val Thr Trp Lys Val Asp Asp Glu Ile Gln Gln
1859 35 40 45
1860
1861 Ser Gly Phe Glu Asn Ser Thr Thr Pro Gln Ser Pro Glu Asp Cys Thr
1862 50 55 60
1863
1864 Tyr Asn Leu Ser Ser Thr Leu Ser Leu Thr Lys Ala Gln Tyr Asn Ser
1865 65 70 75 80
1866
1867 His Ser Val Tyr Thr Cys Glu Val Val His His Asn Ser Gly Ser Ala
1868 85 90 95
1869
1870 Ile Val Gln Ser Phe Asn Arg Gly Asp Cys
1871 100 105
1872

321

320

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1873
1874
1875 (2) INFORMATION FOR SEQ ID NO:45:
1876
1877 (i) SEQUENCE CHARACTERISTICS:
1878 (A) LENGTH: 321 base pairs
1879 (B) TYPE: nucleic acid
1880 (C) STRANDEDNESS: both
1881 (D) TOPOLOGY: linear
1882
1883 (ii) MOLECULE TYPE: cDNA
1884
1885 (iii) HYPOTHETICAL: NO
1886
1887 (iv) ANTI-SENSE: NO
1888
1889
1890 (ix) FEATURE:
1891 (A) NAME/KEY: CDS
1892 (B) LOCATION: 1..321
1893
1894
1895 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
1896
1897 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT GAG CAG 48
1898 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
1899 1 5 10 15
1900
1901 TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC TTC TTG AAC AAC TTC TAC 96
1902 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
1903 20 25 30
1904
1905 CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT GAT GGC AGT GAA CGA CAA 144
1906 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
1907 35 40 45
1908
1909 AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG GAC AGC AAA GAC AGC ACC 192
1910 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
1911 50 55 60
1912
1913 TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC AAG GAC GAG TAT GAA CGA 240
1914 Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
1915 65 70 75 80
1916
1917 CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC AAG ACA TCA ACT TCA CCC 288
1918 His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
1919 85 90 95
1920
1921 ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT TA 321
1922 Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
1923 100 105
1924

← same error

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1925

1926 (2) INFORMATION FOR SEQ ID NO:46:

1927

1928 (i) SEQUENCE CHARACTERISTICS:

1929 (A) LENGTH: 106 amino acids

1930 (B) TYPE: amino acid

1931 (D) TOPOLOGY: linear

1932

1933 (ii) MOLECULE TYPE: protein

1934

1935 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

1936

1937	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	Gln
1938	1				5					10					15	

1939

1940	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu	Asn	Asn	Phe	Tyr
1941				20					25					30		

1942

1943	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	Glu	Arg	Gln
1944			35					40					45			

1945

1946	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	Asp	Ser	Thr
1947		50						55				60				

1948

1949	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	Glu	Tyr	Glu	Arg
1950	65					70					75				80	

1951

1952	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr	Ser	Thr	Ser	Pro
1953				85						90					95	

1954

1955	Ile	Val	Lys	Ser	Phe	Asn	Arg	Asn	Glu	Cys						
1956				100					105							

1957

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/952,640

DATE: 06/27/93
TIME: 13:10:31
S5963

LINE ERROR

ORIGINAL TEXT

28 Wrong application Serial Number
572 Wrong Amino Acid Designator
572 Wrong Amino Acid Designator
572 Wrong Amino Acid Designator
572 Wrong Amino Acid Designator
572 Wrong Amino Acid Designator
572 Wrong Amino Acid Designator
592 Wrong Sequence Number
623
1642 Entered and Calc. Seq. Length differ
1726 Entered and Calc. Seq. Length differ
1810 Entered and Calc. Seq. Length differ
1895 Entered and Calc. Seq. Length differ
11 Number of Sequences Doesn't Equal Actual

(A) APPLICATION NUMBER: US 07/952640
210 215 (2) INFORMA
210 215 (2) INFORMA
210 215 (2) INFORMA
210 215 (2) INFORMA
210 215 (2) INFORMA
210 215 (2) INFORMA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
Sequence 13 missing
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
(iii) NUMBER OF SEQUENCES: 46

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/952,640

DATE: 06/27/93
TIME: 13:10:31
S5963

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/952,640

DATE: 06/27/93
TIME: 13:10:31
S5963

LINE ORIGINAL TEXT

CORRECTED TEXT

1287 (2) INFORMATION FOR SEQ ID NO:31
1307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31
1338 (2) INFORMATION FOR SEQ ID NO:32
1347 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32
1370 (2) INFORMATION FOR SEQ ID NO:33
1390 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33
1421 (2) INFORMATION FOR SEQ ID NO:34
1430 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34
1559 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

(2) INFORMATION FOR SEQ ID NO:31:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
(2) INFORMATION FOR SEQ ID NO:32:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
(2) INFORMATION FOR SEQ ID NO:33:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
(2) INFORMATION FOR SEQ ID NO:34:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: